

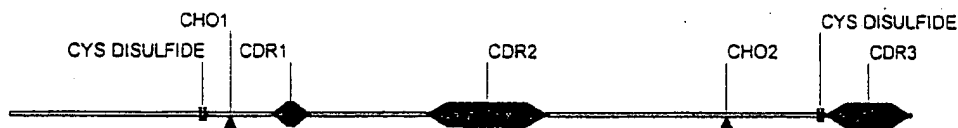
Figure 1A. Alignment of Thy-1 and 8E5 VH

		1		50
EcFv-1.15* 8E5 VH	(1)	-----QEQS--G--AELVKPGASVVMSEKASGYTFNYWM		
Thy1 human	(1)	MNLAISIALLLTLVQVSRGQKVTSLTACLVDQSLRDCRHENTSSSPIQY		
Consensus	(1)	QL	SLKL CK	S S
		51		100
EcFv-1.15* 8E5 VH	(33)	HWVKQEPGGLEWIGTIDPAISYTSYNQNT-----KDKA		
Thy1 human	(51)	ESLTHETKKHVLFGTGVPEHTYRSRTMETSKYHMKVLYLSAFTSKDEE		
Consensus	(51)	F R GTI D NF		KD A
		101		150
EcFv-1.15* 8E5 VH	(67)	TLTVDKPSSSTAYMOESSLTFGDSAVYFCAREEYRYRYFDYNGHGTTEEN		
Thy1 human	(101)	TYTCALHHSGHSPPISSQNVTVLRDKLVKCEGISLLAQNTSWLLLLLESL		
Consensus	(101)	T T S ISS EGI W LSL		
		151 161		
EcFv-1.15* 8E5 VH	(117)	SSAKTEPKT--		
Thy1 human	(151)	SLLOAIDFMSL		
Consensus	(151)	S T L		

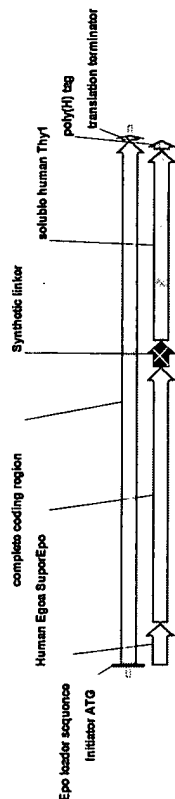
Figure 1B. Design of a single Ig domain CDR binding polypeptide based on the Thy-1 structure.

Qvsrgqkvtsltacldqslrldcrhentsssnym
 Hfsltretkhhvlfgtidpadsytsynqnfkdegtytc
 Alhhsghspissqnvvtvlrdklvkcegvyyryfydy

Figure 1C. Diagram of a single Ig domain CDR carrier based on the Thy-1 structure.



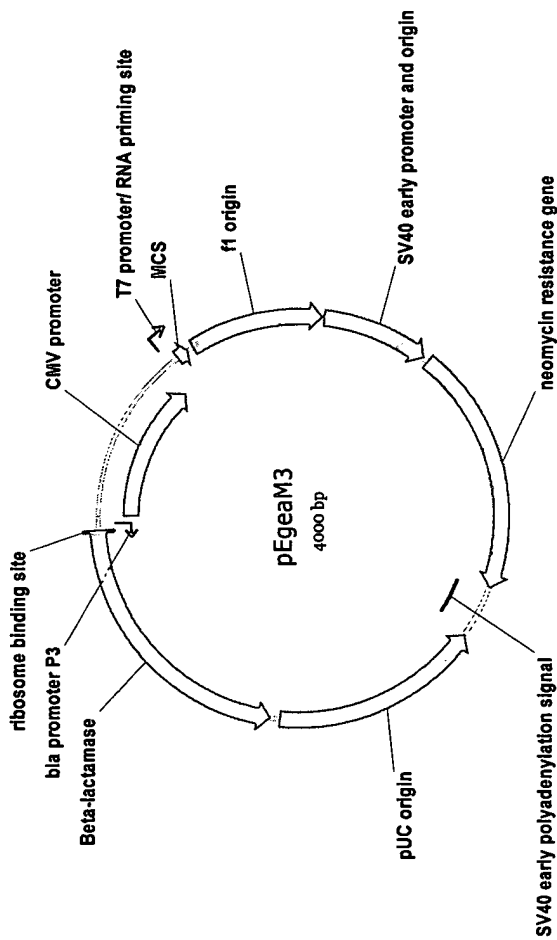
Thy1/8E4 VH synthetic CDR binding polypeptide
 111 aa



EGEA F12 Thy-1 Epo
1050 bp

1 GATTGGCGAA GCTTGGAGGA ATGGCGGTGC ACAGTGCCC CGCTGGCTG TGGCTGCTG TGAGCTGCTG GAGCCTGCTG CCGTGTGGG
CTAACCGCTT CGAACCTCTT TACCCGCACG TGCTCAGCG GCGGACCGAC ACCGACGACG ACTCGGACGA CTCGGAGCGG GACCCGACG GGCACGACCC
101 GlyProPro ArgLeuLeuLeuCys AspSerArg ValLeuGlu ArgHisLeuLeu GluAlaLys GluAlaGlu SerIleThrThr GlyCysVal GluAspCys
CGCCCCCCC CGGCTGATCT GCGACAGCGG GTGTGTGGAG CGGACCTGCG TGGAGGCCAA GGAGGCCGAG AGCATCACA CCGCTGCGT GGAGGACTCG
GCGGGGGGG GCGGACTAGA CGCTGTGCGC CCACGACTC GCGGTGAGC ACCTCCGGT CTCTCCGGCT TCGTAGTGGT GCGCGAGCA CTCTCTGAGC
201 SerLeuAsnGlu AsnIleThr ValProAsp SerLysValAsn PheThrAla TrpLysArg MetLysValGly GlnGlnAla ValGluVal TrpGlnGlyLeu
AGCCTGAACG AGACATCAC CGTCCCCGAC ACAGAGTGA ACTTACGC CTGGAAGCGG ATGGAGGTGG GCACGACGGC CGTGGAGGTG TGGCAGGGCC
TCGGACTTGC TCTGTAGTG GCACGGGCTG TCGTTCACCT TGAAGATGCG GACCTTCGCC TACTCTCCAC CGTCTGTCG GCACCTCCAC ACCGTCCCGG
301 LAlaLeuLeu SerGluAla ValLeuArgGly GlnAlaLeu LeuValIle SerSerGlnPro TrpGluPro LeuGlnLeu HisValAspLys AlaValSer
TGGCCTGCT GAGCAGGCC GTGCTGCGG GCGAGGCCCT GCTGTGTATC AGACCCAGC CTGGGAGCC CTGACAGTG CACGTGGACA AGCCGTGAG
ACGGGACGA CTCGCTCCG CAGCAGGCC CGCTCCGGA GCACACTAG TCGTCGGTCG GGACCTCCG GACGTGCGAC GTGCACCTGT TCCGGCACTC
401 ThrAlaAspThr PheArgLys LeuPheArg AlaLeuArg AlaLeuGly AlaGlnLysGlu AlaIleSer PropoAsp AlaAlaSerAla AlaProLeu ArgThrIle
CGGCTGCGG AGCCTGACCA CCTGTGCG GCGCTGCG GCGCTGCG GCGCTGCG GCGCTGCG GCGCTGCG GCGCTGCG GCGCTGCG GCGCTGCG
GCGGACGCC TCGGACTGGT GGGACGACG GCGGACGCC GCGGACGCC GCGGACGCC GCGGACGCC GCGGACGCC GCGGACGCC GCGGACGCC
501 ThrAlaAspThr PheArgLys LeuPheArg AlaLeuArg AlaLeuGly AlaGlnLysGlu AlaIleSer PropoAsp AlaAlaSerAla AlaProLeu ArgThrIle
ACCGCGACA CTTCCCGGAA GTGTTCGGG GTGTTCGGG GTGTTCGGG GTGTTCGGG GTGTTCGGG GTGTTCGGG GTGTTCGGG GTGTTCGGG
TGGCGGCTGT GGAAGGCCTT CGACAAGGCC CACATGGGT TGAAGGACG CCGGTTCGAC TTCAAGATGT GCGCGTCCG GACGGCCCG CCGCGCCCG
601 GSerGlyGly GlyGlyGly PheGlyGlyGly GlySerGln LysValThr SerLeuThrAla CysLeuVal AspGlnSer LeuArgLeuAsp CysArgHis
GCAGCGCGG CGCGCGCGG TTCCGCGCGG GCGGACGCC GAAGTGACG AGCCTGACG CCTGCTGCT GACCCAGAGC CTGCGGCTGG ACTGCGGCA
CTGCGCGCC GCGCGCGCC AGCGCGCGC GCGCGCGCT CTTCCACTG TCGGACTGG GAGCGGACCA CTTGCTGCT GACCGCGAC TGACGGCCGT
701 GluAsnThr SerSerSerPro IleGlnThr GluPheSer LeuThrArgGlu ThrLysLys HisValLeu PheGlyThrVal GlyValPro GluHisThr
CGAGAACACC AGCAGAGCC CCATCCAGTA CGAGTTCCAG CTGACCGGG AGACAAGAA GCAGTGCTGT TTGCGCACCG TGGCGTGGC CGAGCACACC
GCTCTGTGG TCGTGTGTCG GTTAGTTCAT GCTCAATCG GACTGGGCC TCTGTTCTT CGTGCACGAC AAGCGTGGC ACCCGACGG GCTCGTGTGG
801 TyrArgSerArg ThrAsnPhe ThrSerLys TyrHisMetLys ValLeuLeu ThrSerAla PheThrSerLys AspGlnGly ThrThrThr CysAlaLeuHis
TACCGAGCC GGACCAACT CACAGCAAGT TACCACATGA AGGTGCTGA CTTGACGCC CTTGACGCC CTTGACGCC CTTGACGCC CTTGACGCC
ATGGCTCGG CTGGTTGAA GTGTCGTTC ATGTTGACT TCCAGACAT GGACTCGCG AAGTGGTCT TCTGCTGCC GTGGATGTG ACGGCGGACG
901 HHISerGly HisSerPro ProIleSerSer GlnAsnVal ThrValLeu ArgAspLysLeu ValLysCys GluGlyLe SerLeuLeuAla GlnAsnThr
ACCATCGG CCACAGCCC CCATCAGA GCCAGACGT GACCGTGTG CCGGACAGC TGTGTAAGT CCGAGGATC AGCTGCTGG CCCAGAAC
TGGCTCGC GGTGTGCGG GGTGTGCTG CCGTCTTGA CTGGCAGAC GCGCTGTTG ACCACTTCA GCTCCCGTAG TCGGACGACC GGTCTTGTG
SerHisHis HisHisHisHis
1001 CAGCACCACC CACCACCACC ACTGATGATA AGATCGGATC CTAGGCTTCC
GTGCGTGGTG GTGCTGGTGG TGACTACTAT TCTAGCCTAG GATCGAAGG

FIGURE 3



pEgea M3

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1  GATTATTCTA GACCCGCGTT ACATAACTTA CGGTAATGG CCCGCTGGC TGACCGCCCA ACGACCCCGC CCCATTGACG TCAATAATGA CGTATGTTCC
   CTAATAAGAT CTGGCGGCAA TGTATTGAAT GCATTATTACC GGGCGGACCG ACTGCGGGGT TGGTGGGGG GGGTAACATGC AGTTATTACT GCATACAAGG
   CATAGTAACG CCAATAGGGA CTTTCCATTG AGGTCAATGG GTGGATATTG TACGGTAAAC TGCCCACTTG GCAGTACATC AAGTGTATCA TATGCCAAGT
   GTATCATTGC GGTATCCCTT GAAAGGTAA CACCTATACC TGCGAGTTAC CACCTATACC ATGCCATTTG ACGGTGAAC CGTCATGTAG TTCACATAGT ATACGGTTCA
   ACGCCCCCTA TTGACGTCAA TGACGGTAAA TGCCCGGCTT TGGCCGCTT GGCATATATG CCAATATATG ACCTTATGGG ACTTTCCTAC TTGGCAGTAC ATCTACGTAT
   TGCGGGGGAT AACTGCAGTT ACTGCCATT ACTGCCGCTT TTTGGCAGTA CATCAATGGG GGTTCATGAC TGAATAACCC TGAAGAGATG AACCCATG TAGATGCATA
   TAGTCATCGC TATTACCATG GTGATGCGGT TTTGGCAGTA CACCTATACC GGTTCATGAC TGAATAACCC TGAAGAGATG AACCCATG TAGATGCATA
   ATCAGTAGCG ATATGGTAC CACTACGCCA AAACCGTCAT GTAGTTACCC GCACATATCG CCAACTGAG TGGCCCTAAA TTGACGCAAA TGGCGGTAG CGTGTACGG
   CGTCAATGG AGTTGTTTTT GGCAACCAAA TCAACGGGAC TTTCCAAAT TCGGTAACAA CTCGCGCCCA TCGCGGGGT AACTGCGTTT ACCCGCATC GCACATGCC
   GCAGTTACCC TCAACAAAAA CCGTGGTTTT AGTTGCCCTG AAAGTTTTTA CAGCAATTCAC TACGACTCAC TATAGGGAGA CCAAGCTGG CTAGCGTTTA AACTTAAGCT
   TGGGAGGTCT ATATAAGCAG AGCTCTCTGG TAACTAGAA TCGAATTTAA TACGACTCAC TATAGGGAGA CCAAGCTGG CTAGCGTTTA AACTTAAGCT
   ACCCTCCAGA TATATTCGTC TCAGAGAGAC GATTATCTT AGCTTTAAT ATGTGAGTG CGGCGCATTA AGCGGGGGG GTGTGTGGT TACCGCGAGC GTGACCGCTA
   TGGTACCGGAG CTCGGATCCA CTCTAGGGGG TATCCCGACG CGCCCTGTAG CGGCGCATTA AGCGGGGGG GTGTGTGGT TACCGCGAGC GTGACCGCTA
   ACCATGGCTC GAGCCTAGGT GAGATCCCCC ATAGGGGTGC GCGGACATC GCGCGTAAAT TCGCGCGGCT TCCCGCTCAA GCTCTAATC GGGGGCTCCC
   CACTTGGCAG CGCCTTAGG CCGCTCTCTT TCGCTTCTT CCGCTCTCTT CCGCGCATTA AGCGGGGGG GTGTGTGGT TACCGCGAGC GTGACCGCTA
   GTGAACGGTC GCGGATCCG GGGCGAGGAA AGCGAAGAA GCGAAGGAA GAGCGTGA GAGCGCGGCT TCCCGCTCAA GCTCTAATC GGGGGCTCCC
   TTTAGGTTTC CGATTAGTG CTTTACGGCA CCTCGACCCC AAAAAGTTG ATTAGGGTGA TGGTTCAGT AGTGGGGCAT CGCCCTGATA GACGGTTTTT
   AAATCCCAAG GCTAAATCAC GAAATGCCG GAGAGCTGGG TTTTGTGAAC TAATCCCACT ACCAAGTGA TCACCCGCTA GCGGGACTAT CTGCCAAAAA
   CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCTTGTCCA AACTGGAACA ACACTCAACC CTATCTCGGT CTATTCTTTT GATTTATAAG
   GCGGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACTGT AGAACAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCA GATAAGAAAA CTAATATATC
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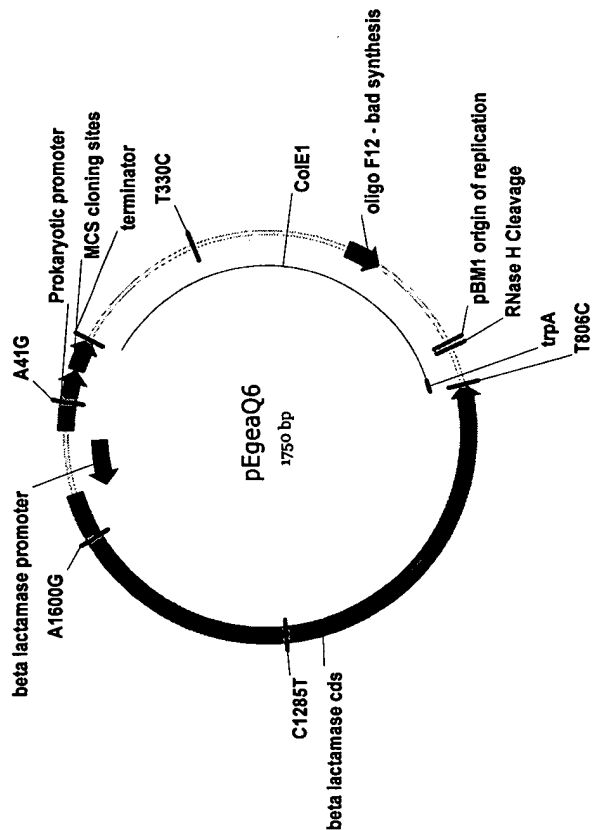
FIGURE 5

1001 GGATTTGGC GATTTGGCC TATTGGTTAA AAAATGAGCT GATTAAACAA AAATTTAAGC CGAATTAAAT CTGTGGAATG TGTGTCAATT AGGTGTGGA
1101 CCTAAACGG CTAAAGCCG ATAAACCAAT TTTTACTCGA CTAATTTGTT TTTAAATTGC GCTTAATFAA GACACTTAC ACACAGTCAA TCCACACCT
1201 AATGCCCAAG GCTCCCCAG AGCAGAGAT ATGCAAGCA TGTACTCAGC ACCAGTCTGT GAAAGTCCCC AGGTCCCCCA GCAGCAGAA
1301 TTACGGGTC CGAGGGTGC TCGTCTTCA TACGTTTCGT ACTAGTAGTT AATCAGTCGT TGTCTCACAT TCCAGGGT TCCAGGGT CGTCGTCTT
1401 GTATGCAAG CATGCATCTC AATATAGTAG CAACCATAGT CCGGCCCTCA ACTCCGCCCA TCCCGCCCT AACTCCGCC AGTTCGCCC ATTCGCCGC
1501 CATAGTTTC GTACGTAGG TTAATCAGTC GTTGGTATCA GGGCGGGAT TGAGCGGGT TGAGCGGGG TCAAGCGGG AGCTTTTGG AGGCTAGGC
1601 CCAATGAGTGA CTAATTTTTT TTAATTATGC AGAGCGGCTC GCGGCTCTG CCTCTGAGT ATCCAGAGT TAGTAGAGT GCTTTTGG AGGCTAGGC
1701 GGTACCGACT GATTAAAAA ATAAATACG TCTCGGCTC CGCGGAGAT GGAGACTCGA CAGCATCTC ATCAGTCTCT CGAAAACCT TCCGATCCG
1801 TTTTCCAAA AGCTCGAGA TCGTTTCGCA TGATTGAACA CGGAGATTG CACGAGTT TCTGCTTTC TAAGCTCTTC ATGACTCTCT GCTATGACTG
1901 AAACGTTTT TCGAGTCTCT AGCAAGGCT ACTAATTTGT TCTACTAAC GTGCTTCAA GAGCGCGG AACCCACTC TCCGATAAGC CGTATGACTG
2001 GGCACACAG ACAATCGGT GCTCTGATGC GCGGTTGTC CCGCTTCTAG CGCAGGGG CGCGTTCTT TTTGTCAAGA CCGACCTGT CCGTCCCCTG
2101 CCGTGTGTC TGTAGCCGA CGAGACTAG GCGGACAAG GCCGACAGT CGTCCCGG GCGCCAGAA AAACAGTTCT GGTGGACAG GCCACGGAC
2201 AATGAAGTC AGGACGAGC AGCGCGGCTA TCGTGCGTGG CCACGACGG CGTTCCTTC GCAGCTGTGC TCGACGTGT CACTGAAGC GGAAGGACT
2301 TTACTTGAG TCTGTCTCG TCGCGCGAT AGCACGACC GGTGTGCCC GCAAGGAAG CGTCGACAG AGCTGCAAC CATCATGCT GATGCAATGC GCGGCTGCA
2401 GGTGCTATT GGGCGAAGT CCGGGCAGG ATCTCTGTG ATCTCACCTT GCTCTGCG AGAAGTATC AGCTGCAAC CATCATGCT GATGCAATGC GCGGCTGCA
2501 CCGAGATAA CCGCTTAC GCGGCTTCA CCACCAAGC AATATGGA TAGATGGA AAACATCGA CCGAGCGC ACCTACTCG ATGGAAGCG GTCTTCTGA TCAGGATGAT
2601 TACGCTTGAT GCGGATGGA CCGGTAACT GGTGTTTCG TTTGTAGCGT AGCTCGCTG AGCTGCGC AGAAGTATC AGCTGCAAC CATCATGCT GATGCAATGC GCGGCTGCA
2701 ATGCGAACA AGCATCAGG GCTCGCGCA GCGGAACTGT TCGCGAGGT CAAGCGCGC ATGCGGCTG TGTCTGAGC TACCTGAGCT TACACTCGTT
2801 GACCTGCTT TCGTAGTCC CGGCTTGA CCGCTTGA AGCTTTCG AGCTGCGC TCGGCTGAG TCGGCTGAG TCGGCTGAG TCGGCTGAG TCGGCTGAG
2901 CCGCTTGC GAATATCAT GTGAAAATG CCGGCTTTC TGAATCAT GACTGTGCG GCTGTGCG GCTGTGCG GCTGTGCG GCTGTGCG GCTGTGCG
3001 GGACGACGG CTTATAGTAC CACCTTTAC CCGGAAAG AGCTTTCG GCAATGAGT GCGGCTTTC TCGTCTTTC CCGTATCGC GCTGTGCG GCTGTGCG GCTGTGCG
3101 TACCGTGAT ATTGCTGAG AGCTTTCG TCGAACCG CCGTACCGA AGCTTTCG GCAATGAGT GCGGCTTTC TCGTCTTTC CCGTATCGC GCTGTGCG GCTGTGCG
3201 CGCTCTTTC TACGAGTCTT CTGAGCGGA GCGACCCCA CTTGTTTAT CAGCTTATA ATGCTTATA ATGCTTATA ATGCTTATA ATGCTTATA ATGCTTATA
3301 GCGGAAGAC TGCTCAAGAA GACTCGCTT CCGTGGGTT GAACATAA CCGTGAATAT TACCAATGT TATTCGTA TCGTAGTGT TAAAGTGT TAAAGTGT
3401 TAAAGCATTT TTTTCACTG ATTTAGTGT TGGTTTCTC AAATCATCA ATGATCTTCA TCAATCTGT ATACCTGCTA ATGCTGCTA ATGCTGCTA
3501 ATTTGCTAAA AAAAGTGAG TAAGATCAAC ACCAAAGG TTTGAGTAGT TACATAGAT AGTACAGACA TATGGAGCT GGAGATCGAT TACACTCGTT
3601 AAGGCCAGCA AAAGCCAGG AACCGTAAA AGCCCGGTT GCTGGGTTT TCCATAGAGT TACATAGAT AGTACAGACA TATGGAGCT GGAGATCGAT TACACTCGTT
3701 TCCGCTCGT TTTCCCGTCC TTGGCATTT TCCGCGCAA AGCTTTCGAG GACCTTCGAG AGGCGGGG ACTGCTGTA GTGTTTTAG CTTGAGTTT
3801 TCAGAGTGG CGAAACCGA CAGGACTATA AAGTACAG CCGTTTCCC CTGGAAGCT CCGTGTGCG TCTCTGTT CCGACCTGCC GCTTACCGGA
3901 AGCTTCCAC GCTTTGGCT TTCTATGAT TTCTATGAT CCGAAAGG GACCTTCGAG GAGAGCAAG AGGAGCAAG GCTTGGGCT GCTTGGGCT GCTTGGGCT
4001 TACCTGTCC CTTTCTCCC TTTGGGAGC GTGGCGTTT CTCATAGTC AGCTGTAG TATCTAGT ATAGAGTCAA GGCACATCCA GCAAGCGAG GCTTGGGCT
4101 ATGACACAGC ACCCCCGTT CAGCCGACC GCTGCGCTT ATCCGTAAC TATGCTTTC AGTCCACCC GGTAAAGAC GACTTATCG CACTGGCAGC
4201 CACACGCTG TGGGGGCAA GTCCGGCTG CAGCGCGAA TAGGCAATG ATAGCAGAC TATGCTTTC GGTGCTGAG TGTATGCTG TGTATGCTG TGTATGCTG
4301 AGCCACTGGT AACAGGATA GCAGAGCGAG GTATGAGG GGTGCTACAG AGTCTTGA AGTCTTGA GGTGCTGAG TGTATGCTG TGTATGCTG TGTATGCTG
4401 TCGGTGACA TTGCTCTAAT CGTCTGCTC CATACTCCG CCACGATGC TCAAGAACT CACCAACGGA TGTATGCTG TGTATGCTG TGTATGCTG TGTATGCTG
4501 GGTATCTGG CTCTGCTGNA GCGATPACC TCCGAAAAG AAGCTTTT CTTCAACATC GAGACTAG GGTCTGAG GGTCTGAG GGTCTGAG GGTCTGAG GGTCTGAG
4601 CCAATGAGT TACCGCAGA AAAAAGAT CTCAAGAGA TCTTGTATG TTTTCTACGG GGTCTGAG GGTCTGAG GGTCTGAG GGTCTGAG GGTCTGAG
4701 TCGTCTGCTA ATGCGCTCT TTTTCTCTA GAGTTCTCT AGTAACTAG AAAAGATG GTTCTGAG TTTTCTACGG GGTCTGAG GGTCTGAG GGTCTGAG GGTCTGAG
4801 TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTTTC TTAATCATA GTTCTGAG TTTCTGAG TTTCTGAG TTTCTGAG TTTCTGAG TTTCTGAG
4901 ATTATGCTACT CCGTGGATAG AGTCTGCTA CAGATAAGC AAGTAGGTAT CAAGGACTG AGGCGCAGCA CATCTATGA CATCTATGA CATCTATGA CATCTATGA
5001 ATCTGGCCCC AGTGTGCAA TGTATCCGG AGACCCAGC TCACCGGCT CAGATTTATC CAGCTATG CAGCTATG CAGCTATG CAGCTATG CAGCTATG
5101 TAGACCGGGT TACGACGCT ACTATGGCG CTCTGGTGG GTCATAATAG TCGTATTTG CCGGTCTGG CCGGTCTGG CCGGTCTGG CCGGTCTGG
5201 GGTCTGTCAA CTTTATCCG CTCATCCAG TCTATTAAT GTTGGCGGA AGCTAGAGTA AGTATGCTG CCGGTCTGG CCGGTCTGG CCGGTCTGG CCGGTCTGG

FIGURE 5B CONT.

3401 CCAGGACGTT GAAATAGGCG GAGTAGGTC AGATAATTAA CAACGGCCCT TCGATCTCAT TCATCAAGCG GTCAATTATC AAACGGCTTG CAACACGGT
TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTG AGCTCCGGTT CCCAACGATC AAGCGGAGTT ACATGATCCC CCATGTTGTG
AACGATGTCC GTAGCACCAC AGTGCAGCA GCAAACCATATA CCGAAGTAAG TCGAGGCCAA GGGTTGCTAG TTCCGCTCAA TGTACTAGG GGTACACAC
3501 CAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCGAGT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT
GTTTTTTCG CAATCGAGGA AGCCAGGAGG CTAGCAACAG TCTTCATTCA ACCGCGCTCA CAATAGTGAG TACCAATACC GTGCGTACGT ATTAAGAGAA
3601 ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCATTG TGAGAATAGT GTATGCCGCG ACCGAGTGC TCTTGCCCGG
TGACAGTACG GTAGGCATTG TAGGAARAAG CACTGACCAC TCATGAGTTG GTTCAGTAAG ACTCTTATCA CATAACGCGC TGGCTCAACG AGAACGGCC
3701 CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTTGAA AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT
GCAGTTATGC CCTATTATGG CCGCGTGTAT CGTCTTGAAA TTTTCACGAG TAGTAACCTT TTGCAAGRAAG CCCCCTTTT GAGAGTTCCT AGAATGGCGA
3801 GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC TGATCTTAC CATCTTTTAC TTTTCCACGAG GTTCTGGGT GAGCAAAAAC AGGAAGGCAA
CAACTCTAGG TCAAGCTACA TTGGGTGAGC ACGTGGGTG ACTAGAGTC GTAGAAATG AAAGTGCTG CAAGACCCA CTCGTTTTG TCCTTCGGTT
3901 AATGCCGCAA AAAAGGGAAT AAGGCGGACA CGAAATGTT GAATACTCAT ACTCTTCCCT TTTCAATAT ATTGAAGCAT TTATCTAGAG GTTATTGTCT
TTACGGCGTT TTTTCCCTTA TTCCCGCTGT GCCTTTACAA CTTATGAGTA TGAGRAGGAA AAAGTTATAA TAACTTCGTA AATAGATCTC CAATAACAGA

FIGURE 5B CONT.



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1  AGTGTCTCTAG  ACCGTGTTGAC  AATTAATCAT  AATGTGTGGA  ATTGTGAGCG  GATAACAAT  TCACACAGGA  AACAGGATCG  ATCGAATTTCG
101 TCACGAGATC  TGGACAACCTG  TTAATTAGTA  GCCGAGCATA  TTACACACCT  TAACACTCGC  CTATTGTTAA  AGTGTGTCTT  TTGTCCTAGC  TAGCTTAAGC
201 GATCCAAGCT  TGAGCTCGAG  CCATGGCCCG  GGTGAATTAAT  TAGAAGAAT  CAAAGGATCT  TCTTGAGATC  CTTTTTTTCT  GCGCGTAATC  TGCTGCTTGC
301 CTAGGTTCTG  ACTCGAGCTC  GGTACCGGSC  CCACCTTATTA  ATCTTTTCTA  GTTTCCTAGA  AGRACCTTAG  GAAAAAAGA  CGCGCATTAG  ACGACGAACG
401 AAACAAAAA  ACCACCGCTA  CCAGCGGTGG  TTTGTTTGGC  GGATCAAGAG  CTACCAACTC  TTTTTCGAA  GGTAACTGGC  TTCAGCAGAG  CGCAGATACC
501 TTTGTTTTT  TGGTGGCGAT  GGTGCGCCAC  AACAAACGG  CCTAGTTCTC  GATGTTTGG  AAAAGGCTT  CCATTGACCG  AAGTCGCTC  CGCTCTATGG
601 AATACTGTT  CTTCTAGTGT  AGCGTAGT  AGGCCACAC  TCAAGAACT  CTGTAGCACC  GCCTACATAC  CTCGCTCTGC  TAATCCTGTT  ACCAGTGGCT
701 TTTATGACAA  GAAGATCACA  TCGGCATCAA  TCCGGTGGTG  AAGTTCTTGA  GACATCGTGG  CGGATGTATG  GAGCGAGACG  AATTAGGCAA  TGGTCACCGA
801 GCTGCCAGTG  GCGATAAGTC  GTGCTTTACC  GGTGTTGACT  CAAGCAGATA  GTTACCGGAT  AAGCGCGCAG  GGTGCGGCTG  AACGGGGGT  TCGTGACACAC
901 CGACGGTCAC  CGCTATTTCAG  CACAGAATGG  CCCAACCTGA  GTTCTGCTAT  CAATGGCCTA  TTCCGCGTCG  CCAGCCCGAC  TTGCCCCCA  AGCAGTGTG
TCCGGTTCGAA  CCTCGCTTGC  TGGATGTGGC  TTGACTCTAT  GGATGTGCGA  CTCGATCTC  TTTGCGGGTG  CGAAGGGCTT  CCCTGTTTC  GCCTGTCCAT
TCCGGTAAGC  GGCAGGGTCG  GAACAGGAGA  GGCACACAGG  GAGCTTCCAG  GGGGAAACGC  CTGCTATCTT  TATAGTCTG  TCGGGTTTCG  CCACCTCTGA
AGGCCATTGC  CCGTCCCAGC  CTTGTCTCT  CCGTGTCTC  CTCGAGGTC  CCCCTTGGC  GACCATAGAA  ATATCAGGAC  AGCCCAAGC  GGTGGAGACT
CTTGAGCGTC  GATTTTGTG  ATGCTCGTCA  GCGGGGGGGA  CCCTATGGAA  AAACGCCAG  AACCGGCTT  TTTTACGGTT  CCTGCCGCT  CATTAGGCGG
GAATTCGCAG  CTAAACACAC  TAGCAGCAGT  CCCCCCGCT  CGGATACCTT  TTTGCGGCG  TTGGCCCGGA  AAAATGCCAA  GGACGGCGGA  GTAATCCGCC
GCTATTACCA  ATGCTTAATC  AGTGAGGCAT  CTATCTCAG  GATCTCTA  TTTCGTTCA  CCAATAGTGC  CTGACTCCCC  GTCGTGTAGA  TAACTACGAT
CGATATGGT  TACGAATTAG  TCACTCCGTG  GATAGATCG  CTAGACAGT  AAAGCAAGTA  GGTATCGAGG  GACTGAGGG  CAGCATATCT  ATTGATGCTA
ACGGAGGGC  TTACCATCTG  GCCCAGTGC  TGCAATGATA  CCGCAGACC  CACGCTCAC  GGCTCCAGAT  TTATCAGCAA  TAAACGAGC  AGCCGGAAGG
TGCCCTCCCG  AATGGTAGAC  CCGGGTCACG  ACGTTACTAT  GCGCTCTTGG  GTGCGAGTGG  CCGAGGTCTA  AATAGTCTGT  ATTTGTCGG  TCGGCTTCC
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FIGURE 6

1001 GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCCTCCA TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG TTCCGCAGTT AATAGTTTGC
1101 CGGCTCGCGT CTTACACAGG ACCTTGAAAT AGCGGGAGGT AGGTGAGATA ATTAACAACG GCCCTTCGAT CTCATTTCATC AAGCGGTCAA TTATCAAAACG
CGAACGTTGT TGCCATTGCT ACAGGCATCG TGGTGTACAG TCGTCTGTTT GGTATGGCTT CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG
1201 CGTTGCAACA ACGGTAAACGA TGTCGGTAGC ACCACAGTGC GAGCAGCAA CCATACCGAA GTAAAGTCCG GCCAAGGTT GCTAGTTCCG CTCATGTATC
ATCCCCCATG TTGTGCAAAA AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTAT CACTCATGGT TATGGCAGCA
1301 TAGGGGTAC AACACGTTTT TTCGCCAATC GAGGAAGCCA GGAGGTAGC AACAGTCTTC ATTCAACCGG CGTCAACTCT GTGAGTACCA ATACCGTCTG
CTGCATAATT CTCTTACTGT CATGCCATCC GTAAAGTGTCT TTTCTGTGAC TCGAGTAC TCAACCAAGT CATTCAGAGA ATAGTGTATG CCGCGACCGA
1401 GACGTATTAA GAGAAATGACA GTACGGTAGG CATTCACGTA AAGACACTG ACCACTCATC TGCTCATCAT TGAACACGT TCTTCGGGGC GAAACTCTC
GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGGCCG TATGCCCTAT TATGGCGCGG TGTATCGTCT TGAATTTTC ACCAGTAGTA ACCTTTTGA AGAAGCCCG CTTTTGAGAG
1501 CAACAGAAC GGGCGCGAGT GATCCAGTTC GATGTAACCC ACTCGTGCTC CCAACTGATC TTGAGCACTT TTTACTTTCA CCAGCGTTTC TGGGTGAGCA
AAGGATCTTA CCGCTGTTGA CTAGGTCAAG CTACATTGGG TGAGCACGAG GGTGACTAG AAGTCGTAGA AAATGAAGT GGTGCAAAAG ACCCACTCGT
1601 AAAACAGGAA GGCAAAATGC CGCAAAAAG GGAATRAGG CGACACGGAA ATGTTGAATA CTCATACCTCT TCCTTTTCA ATATTATGA AGCATTTATC
TTTTGTCCCT CCGTTTAAAG GCGTTTTTC CCTATTCCC GCTGTGCCCT TACAACCTTAT GAGTATGAGA AGGAAAAGT TATAATAACT TCGTAAATAG
1701 AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT CTAGAGGTA
TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA GATCTTCCAT

FIGURE 6B CONT.